

Sequence Listing

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Wood, William I.
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<141> 1999-05-17

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15 <150> US 60/003,491
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 50 55 60
 30 Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro
 65 70 75
 35 Glu Tyr Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp
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 40 Thr Ile Lys Phe Ala Ala Ala His Thr Asn Thr Glu Ile Leu Lys
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 45 Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr
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 50 Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys
 155 160 165
 Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr
 170 175 180
 55 Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly
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Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
 215 220 225

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Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg
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 260 265 270

Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu
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20 Pro Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys
 305 310 315

Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala
 320 325 330

25 Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg
 335 340 345

Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys
 350 355 360

30 Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys
 365 370 375

35 Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Thr Asn
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60 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro

65 70 75

5 Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
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5 Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln
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35 Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro
65 70 75

40 Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu
80 85 90

Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln
95 100 105

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Sequence Listing

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Wood, William I.

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<141> 1999-05-17

<150> US 08/706,054
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<150> US 60/003,491
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65 70 75
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140 145 150
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Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg		
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Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile		
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290	295	300
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305	310	315
Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala		
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335	340	345
Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys		
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<223> Sequence source: VEGE-121

<400> 4

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu
1					5				10					15
Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala
					20			25					30	
Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp
				35				40				45		
Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp
				50				55				60		
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro
				65				70				75		
Ser	Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu
				80				85				90		
Gly	Leu	Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln
				95				100				105		
Ile	Met	Arg	Ile	Lys	Pro	His	Gln	Gly	Gln	His	Ile	Gly	Glu	Met
				110				115				120		
Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp
				125				130				135		
Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys	Pro	Arg	Arg			
				140				145			147			

<210> 5

<211> 149
<212> PRT
<213> Human

<220>

<221> Human
<222> 1-149
<223> Sequence source: PIGE-131

<400> 5

Met	Pro	Val	Met	Arg	Leu	Phe	Pro	Cys	Phe	Leu	Gln	Leu	Leu	Ala
1					5				10					15
Gly	Leu	Ala	Leu	Pro	Ala	Val	Pro	Pro	Gln	Gln	Trp	Ala	Leu	Ser
					20				25				30	
Ala	Gly	Asn	Gly	Ser	Ser	Glu	Val	Glu	Val	Val	Pro	Phe	Gln	Glu
				35				40				45		
Val	Trp	Gly	Arg	Ser	Tyr	Cys	Arg	Ala	Leu	Glu	Arg	Leu	Val	Asp
				50				55				60		
Val	Val	Ser	Glu	Tyr	Pro	Ser	Glu	Val	Glu	His	Met	Phe	Ser	Pro
				65				70				75		
Ser	Cys	Val	Ser	Leu	Leu	Arg	Cys	Thr	Gly	Cys	Cys	Gly	Asp	Glu
				80				85				90		
Asn	Leu	His	Cys	Val	Pro	Val	Glu	Thr	Ala	Asn	Val	Thr	Met	Gln

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95 100 105
Leu Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu
110 115 120
Thr Phe Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu
125 130 135
Lys Met Lys Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg
140 145 149

<210> 6
<211> 299
<212> DNA
<213> Unknown

<220>
<223> Sequence source: EST

<220>
<221> unsure
<222> 74
<223> unknown base

<400> 6
ccgtctacag atgtgggggt tgctgcaata gtgaggggct gcagtgcatt 50
aacaccagca cgagctacct cagnaagacg ttatggaaa ttacagtgcc 100
tctctctcaa ggccccaac cagtaacaat cagtttgcc aatcacactt 150
cctgccatg catgtctaaa ctggatgtt acagacaagt tcattccatt 200
attagacgtt ccctgccagc aacactacca cagtgtcagg cagcgaacaa 250
gacctgcccc accaattaca tgtgaaataa tcacatctgc agatgcctg 299

<210> 7
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Sequence source: synthetic probe

<400> 7
ctgggtttca tgcactgcag cccctcacta ttgcagcaac ccccacatct 50

<210> 8
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> Sequence source: synthetic probe

<400> 8
gcatctgcag atgtgattat tccacatgta attgggtggg caggtcttgt 50

<210> 9
<211> 8
<212> PRT

<213> Human

<220>

<221> Human

<222> 1-8

<223> Sequence source: Flt4 partial sequence

<400> 9

Tyr Ser Met Thr Pro Pro Thr Leu
1 5 8

<210> 10

<211> 9

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-9

<223> Sequence source: Flt4 partial sequence

<400> 10

Ser Leu Arg Arg Arg Gln Gln Gln Asp
1 5 9

<210> 11

<211> 40

<212> PRT

<213> Unknown

<220>

<223> Sequence source: Herpes glycoprotein D partial sequence

<400> 11

Lys Tyr Ala Leu Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn
1 5 10 15

Arg Phe Arg Gly Lys Asp Leu Pro Val Leu Asp Gln Leu Leu Glu
20 25 30

Gly Gly Ala Ala His Tyr Ala Leu Leu Pro
35 40

<210> 12

<211> 13

<212> PRT

<213> Human

<220>

<221> Human

<222> 1-13

<223> Sequence source: partial VRP sequence

<400> 12

Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu
1 5 10 13

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NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: *Diskette submitted was blank*

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

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